Claims

1. A DNA encoding the following protein (a) or (b):

(a) a protein comprising the amino acid sequence represented by SEQ ID NO:2;

(b) a protein comprising an amino acid sequence in which one or several amino acids have been deleted, replaced, or added in the amino acid sequence represented by SEQ ID NO:2 and having an L-rhamnose isomerase activity.

2. A DNA comprising the nucleotide sequence represented by SEQ ID NO:1 or a complementary sequence thereof or a sequence containing a part or the whole of any of these sequences.

3. A DNA hybridizing to the DNA according to Claim 2 under stringent conditions and encoding a protein having an L-rhamnose isomerase activity.

4. The DNA according to Claim 1, 2 or 3, which is L-rhamnose isomerase derived from *Pseudomonas stutzerii*.

5. The DNA according to Claim 4, wherein the L-rhamnose isomerase is an enzyme having the following physicochemical properties:

(i) an action

which catalyzes an isomerization reaction represented by any of the bold black lines in Fig. 7, Fig. 8 and Fig. 9;

(ro) an active pH and an optimal pH

in which the active pH ranges from 7.0 to 10.0 and the

optimal pH is 9.0;

(ha) pH stability

in which it is stable within the pH range of 6.0 to 11.0 in the case where it is kept at 4°C for 1 hour at various pH values;

(ni) an active temperature and an optimal temperature

in which the active temperature ranges from 40 to 65°C and the optimal temperature is 60°C;

(ho) a temperature stability

in which it is stable at 40°C for 10 minutes and remains at 90% or more even at 50°C for 10 minutes;

(he) an effect of a chelating agent

in which its activity is hardly inhibited even if it coexists with EDTA or EGTA, which is a chelating agent, during the measurement of its activity;

(to) an effect of a metal ion

in which about 30% of the activity is inhibited by 1 mM cobalt ion; and

(chi) a molecular weight by the SDS-PAGE method

which is about 43,000.

6. A protein comprising the amino acid sequence represented by SEQ ID NO:2.

7. A protein comprising an amino acid sequence in which one or several amino acids have been deleted, replaced, or added in the amino acid sequence represented by SEQ ID NO:2 and having

an L-rhamnose isomerase activity.

8. The protein according to Claim 6 or 7, wherein the L-rhamnose isomerase activity is specified by the following physicochemical properties:

(i) an action

which catalyzes an isomerization reaction represented by any of the bold black lines in Fig. 7, Fig. 8 and Fig. 9;

(ro) an active pH and an optimal pH

in which the active pH ranges from 7.0 to 10.0 and the optimal pH is 9.0;

(ha) pH stability

in which it is stable within the pH range of 6.0 to 11.0 in the case where it is kept at 4°C for 1 hour at various pH values;

(ni) an active temperature and an optimal temperature

in which the active temperature ranges from 40 to 65°C and the optimal temperature is 60°C;

(ho) a temperature stability

in which it is stable at 40°C for 10 minutes and remains at 90% or more even at 50°C for 10 minutes;

(he) an effect of a chelating agent

in which its activity is hardly inhibited even if it coexists with EDTA or EGTA, which is a chelating agent, during the measurement of its activity;

(to) an effect of a metal ion

in which about 30% of the activity is inhibited by 1 mM cobalt ion; and

(chi) a molecular weight by the SDS-PAGE method which is about 43,000.

9. A fusion protein in which a protein according to Claim 6, 7 or 8 has been bound to a protein translation initiation codon.

10. A recombinant vector containing a DNA according to any one of Claims 1 to 5.

11. A host cell containing an expression system that can express a protein according to Claim 6, 7 or 8.

12. A process for producing a recombinant protein characterized by culturing a host cell containing an expression system according to Claim 11 in a medium and collecting a recombinant protein having an L-rhamnose isomerase activity from the thus obtained culture.

13. A method of applying a correlation diagram in which all the monosaccharides having different number of carbon atoms are linked together based on their production processes and molecular structures (D-form and L-form) shown in Fig. 1 to production of a rare sugar characterized in that the location of a target rare sugar in the overall picture of monosaccharides is understood and thus its optimum production pathway on which a protein according to Claim 6, 7, 8 or 9 is allowed to act is designed.

14. The method according to Claim 13, wherein the production of a rare sugar is mass production of a rare sugar.

15. The method according to Claim 13 or 14, wherein the production of a rare sugar is production of a rare sugar from an unused resource.

16. The method according to Claim 13, 14 or 15, wherein the target rare sugar is a rare sugar whose physiological activity has been identified.